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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:26:03 ; Search time 29.37 Seconds
(without alignments)
23.091 Million cell updates/sec

Title: US-09-331-631A-38
Perfect score: 53
Sequence: 1 CXXXXXXXXXXXXXXXXCXXC 21

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	37	1 TXP3_APTSC	P49368 aptostichus
2	53	100.0	39	1 CYGN_CYGAT	P02785 cygnus atra
3	53	100.0	40	1 MELG_MELGA	P21376 melagris g
4	53	100.0	55	1 M84C_DROME	Q01644 drosophila
5	53	100.0	56	1 AMCI_APIME	P56682 apis mellif
6	53	100.0	57	1 MT2_SCYSE	P02806 scylla serr
7	53	100.0	58	1 MT1_HOMAM	P29499 homarus ame
8	53	100.0	58	1 MT1_SCYSE	P02805 scylla serr
9	53	100.0	58	1 MT2_CALSI	P55950 callinectes
10	53	100.0	58	1 MT_ASTFL	P55951 astacus flu
11	53	100.0	58	1 MT_CARMA	P55948 carcinus ma
12	53	100.0	59	1 MT1_PORPO	P55952 potamon pot
13	53	100.0	59	1 MT1_CALSI	P55949 callinectes
14	53	100.0	62	1 MT1_CANGA	P15113 candida gla
15	53	100.0	63	1 M84A_DROME	Q01642 drosophila
16	53	100.0	68	1 M84D_DROME	Q01645 drosophila
17	53	100.0	70	1 SIX1_LEIOU	P19856 leirurus qui
18	53	100.0	72	1 MT11_MYTED	P80246 mytilus edu
19	53	100.0	72	1 MT12_MYTED	P80247 mytilus edu
20	53	100.0	72	1 MT13_MYTED	P80248 mytilus edu
21	53	100.0	72	1 MT14_MYTED	P80249 mytilus edu
22	53	100.0	74	1 M84B_DROME	Q01643 drosophila
23	53	100.0	83	1 MEX1_DROME	P23487 drosophila
24	53	100.0	88	1 SIX1_ANDAU	P01497 androctonus
25	53	100.0	88	1 SIX1_MESMA	P01668 mesobuthus
26	53	100.0	88	1 SIX2_ANDAU	P15147 androctonus
27	53	100.0	94	1 SIXE_BUTJU	P56637 butorius ju
28	53	100.0	95	1 KRP4_ANAPL	P08335 anas platyr
29	53	100.0	95	1 KRP4_COLLT	P07521 columba liv
30	53	100.0	97	1 KRP4_CHICK	P20308 gallus gall
31	53	100.0	97	1 KRPB_CHICK	P04458 gallus gall
32	53	100.0	97	1 KRFC_CHICK	P02450 gallus gall
33	53	100.0	97	1 KRFD_CHICK	P20307 gallus gall

34	53	100.0	98	1 KRFT_LARNO	P02451 larus novae
35	53	100.0	105	1 YG44_YEAST	P53299 saccharomyc
36	53	100.0	107	1 INB3_CAEL	Q09628 caenorhabdi
37	53	100.0	107	1 TAP1_ANTMA	Q04189 antirrhinum
38	53	100.0	115	1 A62E_DROME	Q46202 drosophila
39	53	100.0	157	1 VES5_RHRYL	P24834 rhesus papl
40	53	100.0	178	1 CHHC_BOMO	P20730 bombyx mori
41	53	100.0	194	1 KRUB_HUMAN	Q75690 homo sapien
42	53	100.0	369	1 PP11_HUMAN	P21128 homo sapien
43	53	100.0	399	1 IGIR_MOUSE	Q60751 mus musculu
44	53	100.0	459	1 VTNC_PTG	P48819 sus scrofa
45	53	100.0	467	1 D4DR_HUMAN	P21917 homo sapien

ALIGNMENTS

RESULT	ID	TXP3_APTSC	STANDARD	PRT	37 AA
AC	P49268:				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	APTOXOXIN III (PARALYTIC PEPTIDE III) (PP III).				
OS	Aptostichus schlingeri (trap-door spider).				
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;				
OC	Mygalomorphae; Cyrtachenidae; Aptostichus.				
RN	[1]				
RP	SEQUENCE:				
RC	TISSUE=VENOM;				
RX	MEDLINE=93069259; PubMed=1440641;				
RA	Skinner W.S., Dennis P.A., Li J.P., Quistad G.B.;				
RT	*Identification of insecticidal peptides from venom of the trap-door spider, Aptostichus schlingeri (Ctenizidae).*				
RT	Toxicon 30:1043-1050(1992).				
RL	CC -I- FUNCTION: IS BOTH PARALYTIC AND LETHAL, WHEN INJECTED INTO				
CC	LEPIDOPTERAN LARVAE. IS A SLOWER ACTING TOXIN, BEING LETHAL AT 24				
CC	HR, BUT NOT PARALYTIC AT 1 HR POST-INJECTION.				
CC	-I- PTM: FOUR DISULFIDE BONDS ARE PRESENT.				
CC	-I- MISCELLANEOUS: LD50 IS 0.50 MG/KG BY SUBCUTANEOUS INJECTION.				
CC	-I- SIMILARITY: TO APTOTOXIN VII.				
KW	Venom: Toxin.				
SC	SEQUENCE 37 AA; 3769 MW; CSD01091694E1908 CRC64;				
QY	1 CXXXXXXXXXXXXXXXXCXXC 21				
DB	15 CGGKCAIWNWNCIGGCSKTC 35				
RESULT	2				
ID	CYGN_CYGAT	STANDARD:	PRT:	39 AA.	
AC	P02785:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-FEB-1994 (Rel. 28, Last annotation update)				
DE	CYGNIN.				
OS	Cygnus atratus (Black swan).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.				
RN	[1]				
RP	SEQUENCE:				
RC	TISSUE=EGG WHITE;				
RX	MEDLINE=84087048; PubMed=6654595;				
RA	Simpson R.J., Morgan F.J.;				
RT	*Isolation and complete amino acid sequence of a basic low molecular weight protein from black swan egg white.*;				

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RL Int. J. Pept. Protein Res. 22:476-481(1983).
CC -I- FUNCTION: NOT KNOWN.
CC -I- SIMILARITY: STRONG, TO TURKEY MELEAGRIN, AND SOME, TO A PART
CC (EXON 9) OF TRANSFERRINS.
DR PIR: A03258; IZMS.
KW Egg white.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 6 33 OR 6-32 (BY SIMILARITY).
FT DISULFID 12 28 BY SIMILARITY.
FT DISULFID 16 32 OR 16-33 (BY SIMILARITY).
SQ SEQUENCE 39 AA: 4452 MW: 805DE270495FB4AA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 39;
Best Local Similarity 19.0%; Pred. No. 42;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXKXXXXXXXXXXXXCXXC 21
DB 12 CSSKCSKADVWSLSDCKEYC 32

RESULT 3
MEIG.MEIGA STANDARD: PRT; 40 AA.
AC P21376;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE MELEAGRIN.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=89340398; PubMed=2760022;
RA Odani S., Koide T., Ono T., Takahashi Y., Suzuki J.-I.;
RT "Covalent structure of a low-molecular-mass protein, meleagrin,
RT present in a turkey (Meleagris gallopavo) ovomucoid preparation.";
RL J. Biochem. 105:660-663(1989).
CC -I- FUNCTION: NOT KNOWN.
CC -I- SIMILARITY: STRONG, TO BLACK SWAN CYGNIN, AND SOME, TO A PART
CC (EXON 9) OF TRANSFERRINS.
DR PIR: JX0070; JX0070.
KW Egg white.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 6 33 OR 6-32.
FT DISULFID 12 28
FT DISULFID 16 32 OR 16-33.
SQ SEQUENCE 40 AA: 4552 MW: 2B6C78FE5B302AA4 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 40;
Best Local Similarity 19.0%; Pred. No. 42;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXKXXXXXXXXXXXXCXXC 21
DB 12 CSSKCSKAEVWVSPDCKVHC 32

RESULT 4
M84C.DROME STANDARD: PRT; 55 AA.
AC Q01644; OSVINO;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MALE SPECIFIC SPERM PROTEIN M84DC.
GN M84DC.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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OC Ephydroidae; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=92102953; PubMed=1684716;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
RT Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
RL of Drosophila melanogaster.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amandites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieux E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Davis A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei L., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -I- TISSUE SPECIFICITY: TESTIS.
CC -I- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -I- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPEPTITIVE C-G-P
CC MOTIFS.
CC -I- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: X67703; CAA47939.1; -
DR EMBL: AE003672; AAF54025.1; -
DR HSSP: P01180; INPO.
DR FLYBASE: FBgn0004174; M84DC.
KM Spermatogenesis; Repeat; Multigene family.
SQ SEQUENCE 55 AA: 5225 MW: 95A12F3AEC8B06C CRC64;

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FT METAL 34 34 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 46 46 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 56 56 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 FT VARIANT 1 1 MISSING (IN MT-11A).
 SO SEQUENCE 58 AA: 6287 MW: EF679CB94975C5F0 CRC64:

Query Match 100.0%; Score 53; DB 1; Length 58;
 Best Local Similarity 19.0%; Pred. No. 54;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 21
 DB 34 CSSECKCTSKESCKSKPC 54

RESULT 10

MT_ASTFL STANDARD; PRT; 58 AA.
 ID MT_ASTFL
 AC P55951;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN (MT).
 OS Astacus fluviatilis (Broad-fingered crayfish) (Astacus astacus).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidae; Astacidae; Astacus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-MIDGUT;
 RX MEDLINE-97079279; PubMed-8921011;
 RA Pedersen S.N., Pedersen K.L., Hoefrup P., Depledge M.H., Knudsen J.;
 "Primary structures of decapod crustacean metallothioneins with
 special emphasis on freshwater and semi-terrestrial species.";
 RT Biochem. J. 319:999-1003(1996).
 RL
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
 ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
 METAL IONS.
 CC -1- INDUCTION: BY CADMIUM.
 CC -1- MASS SPECTROMETRY: MM-5910.8; METHOD-MALDI.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
 DR HSSP; P55949; IDMD.
 DR INTERPRO; IPR002045; -;
 DR PRINTS; PR00856; MTCRUSTACEAN.
 DR METAL-binding; Metal-thiolate cluster; Chelation; Cadmium.
 KW DOMAIN 1 29 ALPHA.
 FT METAL 5 58 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 10 10 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 17 17 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 26 26 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 31 31 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 46 46 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 56 56 CLUSTER A.

FT METAL 57 57 CLUSTER A.
 FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
 CADMIUM CONCENTRATION).
 SO SEQUENCE 58 AA: 5911 MW: 576365B3EE5C7122 CRC64:

Query Match 100.0%; Score 53; DB 1; Length 58;
 Best Local Similarity 19.0%; Pred. No. 54;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXX 21
 DB 34 CTSGCKPSECKACTSKPC 54

RESULT 11

MT_CARMA STANDARD; PRT; 58 AA.
 ID MT_CARMA
 AC P55948;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALLOTHIONEIN (MT).
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-MIDGUT;
 RX MEDLINE-94153337; PubMed-8110201;
 RA Pedersen K.L., Pedersen S.N., Hoefrup P., Andersen J.S.,
 Roeperstorff P., Knudsen J., Depledge M.H.;
 "Purification and characterization of a cadmium-induced
 metallothionein from the shore crab Carcinus maenas (L.).";
 RT Biochem. J. 297:609-614(1994).
 RL
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
 CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
 OF HEAVY-METAL IONS.
 CC -1- INDUCTION: BY CADMIUM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
 DR HSSP; P55949; IDMD.
 DR INTERPRO; IPR002045; -;
 DR PRINTS; PR00856; MTCRUSTACEAN.
 DR METAL-binding; Metal-thiolate cluster; Chelation; Cadmium.
 KW DOMAIN 1 29 ALPHA.
 FT METAL 5 58 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 10 10 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 17 17 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 26 26 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 31 31 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 46 46 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 56 56 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
 CADMIUM CONCENTRATION).
 SO SEQUENCE 58 AA: 6133 MW: 0167CDA2E9C9731D CRC64:

Query Match 100.0%; Score 53; DB 1; Length 58;
 Best Local Similarity 19.0%; Pred. No. 54;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CXXXXXXXXXXXXXXXXX 21
 |::|::|::|::|::|::|::|
 Db 34 CXXGCKCTTKEDCKCTKPC 54

RESULT 12

MT_POTPO STANDARD: PRT: 58 AA.
 AC P55952;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE METALLOTHIONEIN (MT).
 OS Potamon potamios.
 OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Fortuonidea; Georyonidae; Potamon.
 RN [1]
 RP SEQUENCE.

RC TISSUE=MIDGUT;
 RX MEDLINE=97079279; PubMed=8921011;
 RA Pedersen S.N., Pedersen K.L., Hoejrup P., Depledge M.H., Knudsen J.;
 RT Primary structures of decapod crustacean metallothioneins with
 special emphasis on freshwater and semi-terrestrial species.";
 RL Biochem. J. 319:999-1003(1996).
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACHA
 ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-

CC METAL IONS.
 CC -1- INDUCTION: BY CADMIUM.
 CC -1- MASS SPECTROMETRY: MW=6156.8; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.

DR HSSP: P55949; IDMD.
 DR INTERPRO: IPR002045; -;
 DR INTERPRO: IPR003019; -;
 DR PFAM: PF00131; metalthio; 1.
 DR PRINTS: PR00858; MTCRUSTACEAN.

KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.

FT DOMAIN 1 29
 FT METAL 30 58 ALPHA.
 FT METAL 4 5 CLUSTER B.
 FT METAL 5 5 CLUSTER B.
 FT METAL 10 10 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 17 17 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 26 26 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 31 31 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 46 46 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 56 56 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 SQ SEQUENCE 58 AA; 6157 MW; DCB71F9AB4DF779C CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
 Best Local Similarity 19.0%; Pred. No. 54;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CXXXXXXXXXXXXXXXXX 21
 |::|::|::|::|::|::|::|
 Db 34 CXXGCKCKSECKCANCKTGPC 54

RESULT 13
 MT1_CALSI STANDARD: PRT: 59 AA.

AC P55949;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE METALLOTHIONEIN-1 (MT-1) (MT-1B/MT-1A).
 OS Callinectes sapidus (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Fortuonidea; Fortunidae; Callinectes.
 RN [1]
 RP SEQUENCE.

RA MEDLINE=95119049; PubMed=7487904;
 RX Brouwer M., Engild J., Hoexum-Brouwer T., Thøgersen I., Truncali A.;
 RT "Primary structure and tissue-specific expression of blue crab
 (Callinectes sapidus) metallothionein isoforms.";
 RL Biochem. J. 311:617-622(1995).
 RN [2]
 RP STRUCTURE BY NMR.

RA Nardella S.S., Brouwer M., Hua Y., Armitage I.M.;
 RT "Three-dimensional solution structure of Callinectes sapidus
 metallothionein-1 determined by homonuclear and heteronuclear
 magnetic resonance spectroscopy.";
 RL Biochemistry 34:620-631(1995).
 CC -1- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
 CADMIUM.

CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
 CC PDB: IDMC; 07-FEB-95.
 CC PDB: IDMD; 07-FEB-95.
 CC PDB: IDME; 07-FEB-95.
 CC PDB: IDMF; 07-FEB-95.

DR INTERPRO: IPR002045; -;
 DR INTERPRO: IPR003019; -;
 DR PFAM: PF00131; metalthio; 1.
 DR PRINTS: PR00858; MTCRUSTACEAN.

KW 3D-structure; Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium;

FT DOMAIN 1 29
 FT METAL 30 59 ALPHA.
 FT METAL 5 5 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 10 10 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 17 17 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 26 26 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 31 31 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 46 46 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 56 56 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 FT VARIANT 1 1 MISSING (IN MT-1A).
 SQ SEQUENCE 59 AA; 6141 MW; 4398B0A9D1A96D34 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 59;
 Best Local Similarity 19.0%; Pred. No. 55;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CXXXXXXXXXXXXXXXXX 21
 |::|::|::|::|::|::|::|
 Db 34 CXXGCKCATKECKSKTCTGPC 54

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RESULT 14
MT1_CANGA STANDARD; PRT; 62 AA.
ID MT1_CANGA
AC P51113
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-I.
GN MT-I.
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC anamorphic Saccharomycetales; Candida.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90062075; Pubmed=2584191;
RA Mehra R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.;
RT "Candida glabrata metallothioneins. Cloning and sequence of the genes
RT and characterization of proteins."
RL J. Biol. Chem. 264:19747-19753(1989).
RN [2]
RP SEQUENCE OF 1-16.
RX MEDLINE=89057829; Pubmed=3194392;
RA Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
RT "Metal-specific synthesis of two metallothioneins and gamma-glutamyl
RT peptides in Candida glabrata."
RL Proc. Natl. Acad. Sci. U.S.A. 85:8815-8819(1988).
CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
CC SEQUESTRATION OF TOXIC METAL IONS.
CC -1- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER ION
CC IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE BY
CC SILVER BUT NOT BY CADMIUM SALTS.
CC -1- MISCELLANEOUS: MT-I MIGHT BIND APPROXIMATELY 11-12 MOL EQ OF
CC CU(II).
CC -1- SIMILARITY: BELONGS TO FAMILY 9 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J05133; AAA35272.1; -.
DR PIR: A31252; A31252.
DR PIR: A34484; A34484.
DR HSSP: P04355; 4MT2.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Repeat.
FT INIT_MET 0
FT REPEAT 22 29
FT REPEAT 55 62
SQ SEQUENCE 62 AA; 6243 MW; 80D768C06C4AF7A1 CRC64;

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Query Match 100.0%; Score 53; DB 1; Length 62;
Best Local Similarity 19.0%; Pred. No. 56;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

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OY 1 CXXXXXXXXXXXXXXXXXC 21
DB 6 CPNCCSPNCANGCCGCCDC 26

RESULT 15
M84A_DROME STANDARD; PRT; 63 AA.
AC 001642; 09VIA3;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MALE SPECIFIC SPERM PROTEIN M8784DA.
GN M8784DA.

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OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=92102953; Pubmed=1684716;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
RA Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
RT of Drosophila melanogaster."
RL Mech. Dev. 35:143-151(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,
RA Baillet R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher S., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideyang C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchem K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclev J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.-A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCTES.
CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
CC MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC -----
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CC -----
CC EMBL: X67703; CAA47937.1; -.
DR EMBL: AF003672; AAF54022.1; -.
DR HSSP: P01180; INPO.
DR FLYBASE: Fbgn0004172; Mst84da.

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KW Spermatoogenesis; Repeat: Multigene family.
SQ SEQUENCE 63 AA; 5806 MW; BF84CD74CBCEFD3F CRC64;

Query Match 100.0%; Score 53; DB 1; Length 63;
Best Local Similarity 19.0%; Pred. No. 57;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXXXC 21
I::I::I::I::I::I::I
Db 16 CCPCGCGCGCGCGCGCGC 36

Search completed: March 1, 2001, 16:26:04
Job time: 401 sec